(Louisville, TX). These oligonucleotides (15-50 mg/ml) were added to the culture media of growing 3T3T cells for various times up to 9 days and the effect of these treatments on P2P expression was determined by Western blotting using the AC88 antibody to detect P2Ps.

REMARKS

Applicants are providing a clean version of the replacement paragraphs amended in the specification. Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE**". No new matter has been added.

This is intended to supplement the response filed November 5, 2002 to the Office Action mailed September 25, 2002. If any issues remain outstanding, the Examiner is respectfully requested to telephone the undersigned attorney of record for. Applicants believe that no fees are due, however, should this be in

error, please debit Deposit Account No. 07-1185 on which the undersigned is allowed to draw.

Respectfully submitted,

Date: Nov 26, 2002

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

On page 4, please replace the paragraph beginning on line 8 with the following rewritten paragraph:

A description is provided of the cloning and characterization of the P2P cDNA. The result of this effort defined a 5173 base pair cDNA, shown in Figure 6 (SEQ ID No. 2), containing a 4214 base pair open reading frame encoding a 156.9 kDa protein. The deduced amino acid sequence of the P2P open reading frame shows a highly basic protein, i.e., pI 9.6, as predicted. Probes to the P2P cDNA detect a single 8 kb mRNA in murine kidney, liver, testes, lung and other tissues and in growing murine 3T3T mesenchymal stem cells. In contrast, P2P mRNA expression is markedly decreased when 3T3T cells undergo the terminal step in the process of adipocyte differentiation. However, P2P mRNA expression is not repressed in nonterminally differentiated adipocytes suggesting that regulation of P2P expression is associated specifically with terminal differentiation.

On page 7, please replace the paragraph beginning on line 23 with the following rewritten paragraph:

Figure 2 shows P2P cDNA-deduced protein consisting of 1404 amino acids shown in SEQ ID NO:1. A hnRNP-associated domain is encoded by amino acids 853 to 1404 and Rb1 binding domain is encoded by amino acids 753 to 908. Potential nuclear localization signals are present between amino acids 717 to 1323 (underlined) and a cysteine-rich domain resembling a "ring" zinc finger is also present from amino acid 61 to 101 (boxed). The cell division sequence motif (CDSM) from amino acids 79 to 97 (bold) is also shown.

On page 10, please replace the paragraph beginning on line 1 with the following rewritten paragraph:

Figure 6 shows the nucleotide sequence of the P2P cDNA (SEQ ID NO:2). The nucleotide sequence contains an open reading frame and additional 3' and 5' untranslated regions of the P2P cDNA.

On page 18, please replace the paragraph beginning on line 21 with the following rewritten paragraph:

Analysis of this cDNA reveals a single long open reading frame extending from an ATG codon at base 139 to a termination

codon at base 4353. The presence of two in-frame stop codons near the 5' end of the cDNA and several in-frame stop codons at the 3' end of the cDNA suggest that the cDNA contains the entire coding region of the gene. This open reading frame has the potential to code for 1404 amino acids to generate a protein having a predicted molecular mass of 156.9 kDa. The deduced amino acid sequence of the protein is shown in Figure 2 (SEQ ID No. 1). This highly basic protein (pI, 9.6) has multiple potential nuclear localization signals between amino acids 717 and 1323 which is in agreement with previous findings that P2Ps represent a subset of nuclear hnRNP proteins (7). In addition, computer analysis of the sequence of the P2P cDNA-derived open reading frame shows a unique cysteine-rich domain near the amino terminus (amino acids 61 to 101) which closely resembles the consensus sequence of the "ring" class of Zn^{++} finger domains (26) and another domain near the amino terminus (amino acids 79 to 97) that has been implicated in cell growth control, i.e., the cell division sequence motif [CDSM] (27).

On page 24, please replace the paragraph beginning on line 4 with the following rewritten paragraph:

The P2P antisense oligonucleotide [5' CAGCAGGAGCTGTGTT '3 cDNA (3424-3409)] shown by SEQ ID No. 3 and a P2P sense oligonucleotide [5' CTACTAAGCCATCGGC '3 (3560-3575)] shown by SEQ ID No. 4 have been prepared, isolated, and studied, as shown below in Table I. The antisense oligonucleotides are prepared by Jude Labs (Memphis, TN) and BioSynthesis (Louisville, TX). These oligonucleotides (15-50 mg/ml) were added to the culture media of growing 3T3T cells for various times up to 9 days and the effect of these treatments on P2P expression was determined by Western blotting using the AC88 antibody to detect P2Ps.